



SUBSTITUTE SEQUENCE LISTING

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<120> METHOD OF GENETIC MODIFICATION OF A WILD  
TYPE VIRAL SEQUENCE

<130> VANM190.001APC

<140> US 09/743,905

<141> 2001-04-24

<150> EP 98870159.5

<151> 1998-07-10

<150> PCT BE99/00089

<151> 1999-07-09

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> genetically modified TGB-3 viral sequence

<221> CDS

<222> (1)...(399)

<400> 1

atg	gtg	ctt	gtg	gtt	gca	gta	gct	tta	tct	aat	att	gta	ttg	tac	ata	48
Met	Val	Leu	Val	Val	Ala	Val	Ala	Leu	Ser	Asn	Ile	Val	Leu	Tyr	Ile	
1			5					10					15			

gtt	gcc	ggt	tgt	gtt	gtt	gtc	agt	atg	ttg	tac	tca	ccg	ttt	ttc	agc	96
Val	Ala	Gly	Cys	Val	Val	Val	Ser	Met	Leu	Tyr	Ser	Pro	Phe	Phe	Ser	
		20					25					30				

aac	gat	gtt	aaa	gcg	tcc	agc	tat	gcg	gga	gca	att	ttt	aag	ggg	agc	144
Asn	Asp	Val	Lys	Ala	Ser	Ser	Tyr	Ala	Gly	Ala	Ile	Phe	Lys	Gly	Ser	
		35					40				45					

ggc	tgt	atc	atg	gac	agg	aat	tcg	ttt	gct	caa	ttt	ggg	agt	tgc	gat	192
Gly	Cys	Ile	Met	Asp	Arg	Asn	Ser	Phe	Ala	Gln	Phe	Gly	Ser	Cys	Asp	
	50					55				60						

att	cca	aag	cat	gta	gcc	gag	tcc	atc	act	aag	gtt	gcc	acc	aaa	gag	240
Ile	Pro	Lys	His	Val	Ala	Glu	Ser	Ile	Thr	Lys	Val	Ala	Thr	Lys	Glu	
	65				70					75					80	

cac gat gtt gac ata atg gta aaa agg ggt gaa gtg acc gtt cgt gtt	288
His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val	
85 90 95	
gtg act ctc acc gaa act att ttt ata ata tta tct aga ttg ttt ggt	336
Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly	
100 105 110	
ttg gcg gtg ttt ttg ttc atg ata tgt tta atg tct ata gtt tgg ttt	384
Leu Ala Val Phe Leu Phe Met Ile Cys Leu Met Ser Ile Val Trp Phe	
115 120 125	
tgg tat cat aga taa	399
Trp Tyr His Arg *	
130	

<210> 2  
 <211> 132  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> genetically modified TGB-3 viral sequence

<400> 2
Met Val Leu Val Val Ala Val Ala Leu Ser Asn Ile Val Leu Tyr Ile
1 5 10 15
Val Ala Gly Cys Val Val Val Ser Met Leu Tyr Ser Pro Phe Phe Ser
20 25 30
Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser
35 40 45
Gly Cys Ile Met Asp Arg Asn Ser Phe Ala Gln Phe Gly Ser Cys Asp
50 55 60
Ile Pro Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu
65 70 75 80
His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val
85 90 95
Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly
100 105 110
Leu Ala Val Phe Leu Phe Met Ile Cys Leu Met Ser Ile Val Trp Phe
115 120 125
Trp Tyr His Arg
130

<210> 3  
 <211> 399  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> genetically modified TGB-3 viral sequence

<221> CDS  
 <222> (1)...(399)

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<400> 3
atg gtg ctt gtg gtt aaa gta gat tta tct aat att gta ttg tac ata 48
Met Val Leu Val Val Lys Val Asp Leu Ser Asn Ile Val Leu Tyr Ile
1 5 10 15

gtt gcc ggt tgt gtt gtt gtc agt atg ttg tac tca ccg ttt ttc agc 96
Val Ala Gly Cys Val Val Val Ser Met Leu Tyr Ser Pro Phe Phe Ser
20 25 30

aac gat gtt aaa gcg tcc agc tat gcg gga gca att ttt aag ggg agc 144
Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser
35 40 45

ggc tgt atc atg gcc gcg aat tcg ttt gct caa ttt ggg agt tgc gat 192
Gly Cys Ile Met Ala Ala Asn Ser Phe Ala Gln Phe Gly Ser Cys Asp
50 55 60

att cca aag cat gta gcc gag tcc atc act aag gtt gcc acc aaa gag 240
Ile Pro Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu
65 70 75 80

cac gat gtt gac ata atg gta aaa agg ggt gaa gtg acc gtt cgt gtt 288
His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val
85 90 95

gtg act ctc acc gaa act att ttt ata ata tta tct aga ttg ttt ggt 336
Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly
100 105 110

ttg gcg gtg ttt ttg ttc atg ata tgt tta atg tct ata gtt tgg ttt 384
Leu Ala Val Phe Leu Phe Met Ile Cys Leu Met Ser Ile Val Trp Phe
115 120 125

tgg tat cat aga taa 399
Trp Tyr His Arg *
130

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<210> 4
<211> 132
<212> PRT
<213> Artificial Sequence

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<220>
<223> genetically modified TGB-3 viral sequence

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<400> 4
Met Val Leu Val Val Lys Val Asp Leu Ser Asn Ile Val Leu Tyr Ile
1 5 10 15
Val Ala Gly Cys Val Val Val Ser Met Leu Tyr Ser Pro Phe Phe Ser
20 25 30
Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser
35 40 45
Gly Cys Ile Met Ala Ala Asn Ser Phe Ala Gln Phe Gly Ser Cys Asp
50 55 60
Ile Pro Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu

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65				70					75				80
His	Asp	Val	Asp	Ile	Met	Val	Lys	Arg	Gly	Glu	Val	Thr	Val
				85					90				95
Val	Thr	Leu	Thr	Glu	Thr	Ile	Phe	Ile	Ile	Leu	Ser	Arg	Leu
				100				105					110
Leu	Ala	Val	Phe	Leu	Phe	Met	Ile	Cys	Leu	Met	Ser	Ile	Val
				115			120					125	
Trp	Tyr	His	Arg										
	130												

<210> 5

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> genetically modified TGB-3 viral sequence

<221> CDS

<222> (1)...(399)

<400> 5

atg	gtg	ctt	gtg	ggt	aaa	gta	gat	tta	tct	aat	att	gta	ttg	tac	ata	48
Met	Val	Leu	Val	Val	Lys	Val	Asp	Leu	Ser	Asn	Ile	Val	Leu	Tyr	Ile	
1				5					10					15		

ggt	gcc	ggt	tgt	ggt	ggt	gtc	agt	atg	ttg	tac	tca	ccg	ttt	ttc	agc	96
Val	Ala	Gly	Cys	Val	Val	Val	Ser	Met	Leu	Tyr	Ser	Pro	Phe	Phe	Ser	
			20					25					30			

aac	gat	ggt	aaa	gcg	tcc	agc	tat	gcg	gga	gca	att	ttt	aag	ggg	agc	144
Asn	Asp	Val	Lys	Ala	Ser	Ser	Tyr	Ala	Gly	Ala	Ile	Phe	Lys	Gly	Ser	
		35					40					45				

ggc	tgt	atc	atg	gac	agg	aat	tcg	ttt	gct	caa	ttt	ggg	agt	tgc	gat	192
Gly	Cys	Ile	Met	Asp	Arg	Asn	Ser	Phe	Ala	Gln	Phe	Gly	Ser	Cys	Asp	
	50					55					60					

att	cca	aag	cat	gta	gcc	gag	tcc	atc	act	aag	ggt	gcc	acc	aaa	gag	240
Ile	Pro	Lys	His	Val	Ala	Glu	Ser	Ile	Thr	Lys	Val	Ala	Thr	Lys	Glu	
	65				70				75						80	

cac	gat	ggt	gac	ata	atg	gta	aaa	agg	ggt	gaa	gtg	acc	ggt	cgt	ggt	288
His	Asp	Val	Asp	Ile	Met	Val	Lys	Arg	Gly	Glu	Val	Thr	Val	Arg	Val	
				85					90					95		

gtg	act	ctc	acc	gaa	act	att	ttt	ata	ata	tta	tct	aga	ttg	ttt	ggt	336
Val	Thr	Leu	Thr	Glu	Thr	Ile	Phe	Ile	Ile	Leu	Ser	Arg	Leu	Phe	Gly	
			100					105					110			

ttg	gat	gat	ttt	ttg	ttc	atg	ata	tgt	tta	atg	tct	ata	ggt	tgg	ttt	384
Leu	Asp	Asp	Phe	Leu	Phe	Met	Ile	Cys	Leu	Met	Ser	Ile	Val	Trp	Phe	
			115				120					125				

tgg	tat	cat	aga	taa												399
Trp	Tyr	His	Arg	*												

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<210> 6  
 <211> 132  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> genetically modified TGB-3 viral sequence

<400> 6  
 Met Val Leu Val Val Lys Val Asp Leu Ser Asn Ile Val Leu Tyr Ile  
 1 5 10 15  
 Val Ala Gly Cys Val Val Val Ser Met Leu Tyr Ser Pro Phe Phe Ser  
 20 25 30  
 Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser  
 35 40 45  
 Gly Cys Ile Met Asp Arg Asn Ser Phe Ala Gln Phe Gly Ser Cys Asp  
 50 55 60  
 Ile Pro Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu  
 65 70 75 80  
 His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val  
 85 90 95  
 Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly  
 100 105 110  
 Leu Asp Asp Phe Leu Phe Met Ile Cys Leu Met Ser Ile Val Trp Phe  
 115 120 125  
 Trp Tyr His Arg  
 130

<210> 7  
 <211> 399  
 <212> DNA  
 <213> Beet Necrotic Yellow Vein Virus

<220>  
 <223> Nucleotide sequence of BNYVV RNA-2 encoding P15  
 protein

<221> CDS  
 <222> (1)...(399)

<400> 7  
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 Met Val Leu Val Val Lys Val Asp Leu Ser Asn Ile Val Leu Tyr Ile  
 1 5 10 15  
 gtt gcc ggt tgt gtt gtt gtc agt atg ttg tac tca ccc ttt ttc agc 96  
 Val Ala Gly Cys Val Val Val Ser Met Leu Tyr Ser Pro Phe Phe Ser  
 20 25 30  
 aac gat gtt aaa gcg tcc agc tat gcg gga gca att ttt aag ggg agc 144  
 Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser  
 35 40 45

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ggc tgt atc atg gac agg aat tcg ttt gct caa ttt ggg agt tgc gat 192
Gly Cys Ile Met Asp Arg Asn Ser Phe Ala Gln Phe Gly Ser Cys Asp
    50                55                60

att cca aag cat gta gcc gag tcc atc act aag gtt gcc acc aaa gag 240
Ile Pro Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu
    65                70                75                80

cac gat gtt gac ata atg gta aaa agg ggt gaa gtc acc gtt cgt gtt 288
His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val
                85                90                95

gtg act ctc acc gaa act att ttt ata ata tta tct aga ttg ttt ggt 336
Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly
                100                105                110

ttg gcg gtg ttt ttg ttc atg ata tgt tta atg tct ata gtt tgg ttt 384
Leu Ala Val Phe Leu Phe Met Ile Cys Leu Met Ser Ile Val Trp Phe
                115                120                125

tgg tat cat aga taa 399
Trp Tyr His Arg *
    130

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<210> 8
<211> 132
<212> PRT
<213> Beet Necrotic Yellow Vein Virus

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<220>
<223> Protein encoded by SEQ ID NO:7

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<400> 8
Met Val Leu Val Val Lys Val Asp Leu Ser Asn Ile Val Leu Tyr Ile
  1                5                10                15
Val Ala Gly Cys Val Val Val Ser Met Leu Tyr Ser Pro Phe Phe Ser
                20                25                30
Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser
                35                40                45
Gly Cys Ile Met Asp Arg Asn Ser Phe Ala Gln Phe Gly Ser Cys Asp
    50                55                60
Ile Pro Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu
    65                70                75                80
His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val
                85                90                95
Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly
                100                105                110
Leu Ala Val Phe Leu Phe Met Ile Cys Leu Met Ser Ile Val Trp Phe
                115                120                125
Trp Tyr His Arg
    130

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